described by Bouwmeester *et al.*, 1996 using the following primer set that amplifies a XNle fragment of 135 bp; F 5'-CAC CAG ATA AAC TGC AGT TAG-3' (SEQ ID NO: 15), R 5'-CTG TTT CAA CTG ATT GCT TCT-3' (SEQ ID NO: 16) (28 cycles).

Please substitute the attached sequence listing for the sequence listing in the application as filed and in the preliminary amendment filed on May 2, 2001.

REMARKS

Applicants submit herewith Sequence Listing substitute pages 1-12 to include as a Sequence Listing as part of this Application.

Applications have amended the Application to include the sequence identification number for SEQ ID Nos. 8-16 in the specification where reference is made to the sequence by use of the assigned identifier as required by 37 CFR §1.812(d). No new matter has been added by virtue of the amendment made to the specification.

Further enclosed is a computer readable copy of the above-mentioned copy of the Sequence Listing. That copy is the same as the copy of the Sequence listing.

Also enclosed is a Statement in Support of Filing and Submissions in Accordance with 37 CFR 1.821-1.825, which declares that the content of the paper and the computer readable copies of the Sequence Listing submitted in accordance with 37 CFR 1.821 (c) and (e), respectively, are the same and that the submission, filed in accordance with 37 CFR 1.821 (g).

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STATEMENT UNDER 37 CFR §1.825(a)

I hereby state that the substitute sheets, which include the Sequence Listing are supported in the Application as filed. I hereby state that the substitute sheets do not include new matter.

The Commissioner is hereby authorized to charge any fees which may be required to consider this submission to Deposit Account No. **04-1105.**

Respectfully submitted,

Date: <u>January 14, 2002</u>

BOS2_17767.1

By: /s/ Cara Z. Lowen
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VERSION WITH MARKINGS TO SHOW CHANGES MADE

IN THE SPECIFICATION:

The paragraph at page 16, lines 11-22 has been amended as follows:

A 15Kb *Sal*I genomic fragment of phage Y2-6 was inserted into the *Xho*I site of the transformation vector pCaSpeR4. UAS-*Nle* was prepared by closing the 1.5Kb *Nle* cDNA as a *Not*I-*Xho*I fragment into pUAST (Brand and Perrimon, 1993). An HA-tagged version of Nle was generated by introducing three copies of the HA epitope (YPUDVPDYA) (SEQ ID NO: 8) immediately downstream of the first Methionine residue. The *Bam*HI-*Asc*I fragment of pKS-Nle was replaced by a corresponding PCR fragment amplified using the following primers:

5' CGGATCCAAA AAATGTATCC CTATGACGTC CCCGATTATG CCTACCCTTA CGATGTACCT GACTACGCGT ATCCGTACGA CGTTCCGGAC TATGCTCAGG AGACGGACA CGGAGCAAGA GGCCACGCCA CATACGATAC AGGCGCGCCA A 3' (SEQ ID NO: 9), and

5' TAAACGAGGC GCGCCTATCG TAT 3' (SEQ ID NO: 10).

The paragraph at page 22, lines 18-22 has been amended as follows:

XNle was isolated by PCR using the degenerate primers, F 5'-CGC AGA ATT CCI TTY GAY GTI CCI GTI GAY AT-3' (SEQ ID NO: 11) and R 5'-GGT GCT CGA GCY TGI GGY TGR TAI ATD ATR TC-3' (SEQ ID NO: 12), designed against conserved peptides, PFDVPVDI (SEQ ID NO: 13) and DIIYQPQ (SEQ ID NO: 14) respectively, found in the Nle domain of the vertebrate proteins identified as expressed sequence tags.

The paragraph at page 22, line 23 to page 23, line 2 has been amended as follows:

Phage stock of a stage 30 library (Stratagene) was used as template to amplify a 200bp fragment that spans Nle domain. Five independent clones were sequenced and found to be identical. This fragment was used to screen the stage 30 library, which resulted in the isolation of 25 positive clones of which the longest of 2.2Kb was sequenced on both strands. Temporal expression was assayed by RT-PCR analysis as described by Bouwmeester *et al.*, 1996 using the following primer set that amplifies a XNle fragment of 135 bp; F 5'-CAC CAG ATA AAC TGC AGT TAG-3' (SEQ ID NO: 15), R 5'-CTG TTT CAA CTG ATT GCT TCT-3' (SEQ ID NO: 16) (28 cycles).

The attached sequence listing has been substituted for the sequence listing in the application as filed and in the preliminary amendment filed on May 2, 2001.